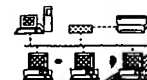


Handled

BIOTECHNOLOGY
SYSTEMS
BRANCH



#8 1/2

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/339,922

Source: 1644

Date Processed by STIC: 9/26/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

1644

RAW SEQUENCE LISTING DATE: 09/26/2000
PATENT APPLICATION: US/09/339,922 TIME: 08:04:08

Input Set : A:\Ix35361.app
Output Set: N:\CRF3\09262000\I339922.raw

**Does Not Comply
Corrected Diskette Needed**

```

3 <110> APPLICANT: Huse, William D.
4 Wu, Herren
6 <120> TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
7 Acids Encoding Same and Methods of Use
9 <130> FILE REFERENCE: P-IX 3536
11 <140> CURRENT APPLICATION NUMBER: US 09/339,922
12 <141> CURRENT FILING DATE: 1999-06-24
14 <160> NUMBER OF SEQ ID NOS: 112
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 351
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(351)
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
29 antibody variable region
31 <400> SEQUENCE: 1
32 cag gtg cag ctg gtg gag tct ggg gga ggc gtt gtg cag cct gga agg 48
33 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg
34 1 5 10 15
36 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat 96
37 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
38 20 25 30
40 gac atg tct tgg gtt cgc cag gct ccg ggc aag ggt ctg gag tgg gtc 144
41 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
42 35 40 45
44 gca aaa gtt agt agt ggt ggt ggt agc acc tac tat tta gac act gtg 192
45 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
46 50 55 60
48 cag ggc cga ttc acc atc tcc aga gac aat agt aag aac acc cta tac 240
49 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
50 65 70 75 80
52 ctg caa atg aac tct ctg aga gcc gag gac aca gcc gtg tat tac tgt 288
53 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
54 85 90 95
56 gca aga cat aac tac ggc agt ttt gct tac tgg ggc caa ggg act aca 336
57 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
58 100 105 110
60 gtg act gtt tct agt 351
61 Val Thr Val Ser Ser
62 115
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 117
67 <212> TYPE: PRT

```

see
pp 2, 3, 5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/339,922

DATE: 09/26/2000
TIME: 08:04:08

Input Set : A:\Ix35361.app
Output Set: N:\CRF3\09262000\I339922.raw

*please insert <223>
at the beginning of
each line
in
that
section;
otherwise,
the lines
are not
shown as
processed
Sequence
Listing.*

68 <213> ORGANISM: Artificial Sequence
69 <220> FEATURE:
69 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
72 <400> SEQUENCE: 2
73 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
74 1 5 10 15
76 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
77 20 25 30
79 Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
80 35 40 45
82 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
83 50 55 60
85 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
86 65 70 75 80
88 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
89 85 90 95
91 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
92 100 105 110
94 Val Thr Val Ser Ser
95 115
99 <210> SEQ ID NO: 3
100 <211> LENGTH: 321
101 <212> TYPE: DNA
102 <213> ORGANISM: Artificial Sequence
104 <220> FEATURE:
105 <221> NAME/KEY: CDS
106 <222> LOCATION: (1)..(321)
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
110 antibody variable region
112 <400> SEQUENCE: 3
113 gag att gtg cta act cag tct cca gcc acc ctg tct ctc agc cca gga 48
114 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
115 1 5 10 15
117 gaa agg gcg act ctt tcc tgc cag gcc agc caa agt att agc aac cac 96
118 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
119 20 25 30
121 cta cac tgg tat caa caa agg cct ggt caa gcc cca agg ctt ctc atc 144
122 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
123 35 40 45
125 aag tat cgt tcc cag tcc atc tct ggg atc ccc gcc agg ttc agt ggc 192
126 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
127 50 55 60
129 agt gga tca ggg aca gat ttc acc ctc act atc tcc agt ctg gag cct 240
130 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
131 65 70 75 80
133 gaa gat ttt gca gtc tat tac tgt caa cag agt ggc agc tgg cct cac 288
134 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
135 85 90 95

*per 1.823 of new sequence rules,
<220> is mandatory
whenever <221>,
<222>, or <223>
is present.*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING

DATE: 09/26/2000

PATENT APPLICATION: US/09/339,922

TIME: 08:04:08

Input Set : A:\Ix35361.app

Output Set: N:\CRF3\09262000\I339922.raw

137 acg ttc gga ggg ggg acc aag gtg gaa att aag 321
 138 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 139 100 105
 142 <210> SEQ ID NO: 4
 143 <211> LENGTH: 107
 144 <212> TYPE: PRT
 145 <213> ORGANISM: Artificial Sequence *same env*
 W--> 146 <220> FEATURE:
 146 <223> OTHER INFORMATION: Description of Artificial Sequence: grafted
 149 <400> SEQUENCE: 4
 150 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 151 1 5 10 15
 153 Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
 154 20 25 30
 156 Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
 157 35 40 45
 159 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
 160 50 55 60
 162 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 163 65 70 75 80
 165 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
 166 85 90 95
 168 Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 169 100 105
 173 <210> SEQ ID NO: 5
 174 <211> LENGTH: 351
 175 <212> TYPE: DNA
 176 <213> ORGANISM: Mus musculus
 178 <220> FEATURE:
 179 <221> NAME/KEY: CDS
 180 <222> LOCATION: (1)..(351)
 182 <400> SEQUENCE: 5
 183 gaa gtg cag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga agg 48
 184 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
 185 1 5 10 15
 187 tcc ctg aga ctc tcc tgt gca gcc tct gga ttc gct ttc agt agc tat 96
 188 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
 189 20 25 30
 191 gac atg tct tgg gtt cgc cag att ccg gag aag agg ctg gag tgg gtc 144
 192 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
 193 35 40 45
 195 gca aaa gtt agt agt ggt ggt agc acc tac tat tta gac act gtg 192
 196 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
 197 50 55 60
 199 cag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc cta tac 240
 200 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 201 65 70 75 80
 203 ctg caa atg agc agt ctg aac tct gag gac aca gcc atg tat tac tgt 288
 204 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys

*insert
2237
at
beginning
of each
line*

RAW SEQUENCE LISTING

DATE: 09/26/2000

PATENT APPLICATION: US/09/339,922

TIME: 08:04:08

Input Set : A:\Ix35361.app

Output Set: N:\CRF3\09262000\I339922.raw

```

205                               85                               90                               95
207 gca aga cat aac tac ggc agt ttt gct tac tgg ggc caa ggg act ctg 336
208 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
209                               100                               105                               110
211 gtc act gtc tct gca 351
212 Val Thr Val Ser Ala
213                               115
216 <210> SEQ ID NO: 6
217 <211> LENGTH: 117
218 <212> TYPE: PRT
219 <213> ORGANISM: Mus musculus
221 <400> SEQUENCE: 6
222 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
223 1 5 10 15
225 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
226 20 25 30
228 Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
229 35 40 45
231 Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
232 50 55 60
234 Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
235 65 70 75 80
237 Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
238 85 90 95
240 Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
241 100 105 110
243 Val Thr Val Ser Ala
244 115
248 <210> SEQ ID NO: 7
249 <211> LENGTH: 321
250 <212> TYPE: DNA
251 <213> ORGANISM: Mus musculus
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)..(321)
257 <400> SEQUENCE: 7
258 gat att gtg cta act cag tct cca gcc acc ctg tct gtg aca cca gga 48
259 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
260 1 5 10 15
262 gat agc gtc agt ctt tcc tgc cag gcc agc caa agt att agc aac cac 96
263 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
264 20 25 30
266 cta cac tgg tat caa caa aaa tca cat gag tct cca agg ctt ctc atc 144
267 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
268 35 40 45
270 aag tat cgt tcc cag tcc atc tct ggg atc ccc tcc agg ttc agt ggc 192
271 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
272 50 55 60
274 agt gga tca ggg aca gat ttc gct ctc agt atc aac agt gtg gag act 240

```

RAW SEQUENCE LISTING

DATE: 09/26/2000

PATENT APPLICATION: US/09/339,922

TIME: 08:04:08

Input Set : A:\Ix35361.app

Output Set: N:\CRF3\09262000\I339922.raw

```

275 Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
276 65 70 75 80
278 gaa gat ttt gga atg tat ttc tgt caa cag agt ggc agc tgg cct cac 288
279 Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
280 85 90 95
282 acg ttc gga ggg ggg acc aag ctg gaa att aag 321
283 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
284 100 105
287 <210> SEQ ID NO: 8
288 <211> LENGTH: 107
289 <212> TYPE: PRT
290 <213> ORGANISM: Mus musculus
292 <400> SEQUENCE: 8
293 Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
294 1 5 10 15
296 Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
297 20 25 30
299 Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
300 35 40 45
302 Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
303 50 55 60
305 Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
306 65 70 75 80
308 Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
309 85 90 95
311 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
312 100 105
316 <210> SEQ ID NO: 9
317 <211> LENGTH: 84
318 <212> TYPE: DNA
319 <213> ORGANISM: Artificial Sequence
321 <220> FEATURE:
322 <223> OTHER INFORMATION: Description of Artificial Sequence:
323 oligonucleotide
325 <400> SEQUENCE: 9
326 caggtgcagc tgggtggagtc tgggggaggc gttgtgcagc ctggaaggtc cctgagactc 60
327 tcctgtgcag cctctggatt cacc 84
330 <210> SEQ ID NO: 10
331 <211> LENGTH: 84
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Description of Artificial Sequence:
337 oligonucleotide
339 <400> SEQUENCE: 10
340 aacttttgcg acccactcca gacccttgcc cggagcctgg cgaaccaag acatgtcata 60
341 gctactgaag gtgaatccag aggc 84
344 <210> SEQ ID NO: 11
345 <211> LENGTH: 87

```

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/339,922

DATE: 09/26/2000
TIME: 08:04:09

Input Set : A:\Ix35361.app
Output Set: N:\CRF3\09262000\I339922.raw

L:69 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:146 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:618 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:886 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:918 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:950 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:982 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1014 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1046 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1078 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1110 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1142 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1174 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1206 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1238 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1270 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1302 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1334 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1366 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1398 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1430 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1462 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1494 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1526 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1558 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1590 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1622 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1654 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1686 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1718 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1753 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1791 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1826 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1858 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1890 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:1922 M:258 W: Mandatory Feature missing, <220> FEATURE: